

Figure 1A

1 CCCACGCGTCCGATTAAAGTGAGGAGAGAGCTACAACCAAGTAAGCAAGTGTCAAGGGCTC 60
 61 ACCAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCAA 120
 1 M Q G Q G R R R G T C K D I F C S K 18
 121 AATGGCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTG 180
 19 M A S Y L Y G V L F A V G L C A P I Y C 38
 181 TGTGTCCCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCC 240
 39 V S P A N A P S A Y P R P S S T K S T P 58
 241 TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGT 300
 59 A S Q V Y S L N T D F A F R L Y R R L V 78
 301 TTTGGAGACCCCGAGTCAGAACATCTTCTCTCCCCTGTGAGTGTCTCCACTTCCCTGGC 360
 79 L E T P S Q N I F F S P V S V S T S L A 98
 361 CATGCTCTCCCTTGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTT 420
 99 M L S L G A H S V T K T Q I L Q G L G F 118
 421 CAACCTCACACACACACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACCTC 480
 119 N L T H T P E S A I H Q G F Q H L V H S 138
 481 ACTGACTGTTCACAGCAAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAA 540
 139 L T V P S K D L T L K M G S A L F V K K 158
 541 GGAGCTGCAGCTGCAGGCAAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGT 600
 159 E L Q L Q A N F L G N V K R L Y E A E V 178
 601 CTTTTCTACAGATTTCTCCAACCCCTCCATTGCCAGGCGAGGATCAACAGCCATGTGAA 660
 179 F S T D F S N P S I A Q A R I N S H V K 198
 661 AAAGAAGACCCAAGGGAAGGTTGTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCAT 720
 199 K K T Q G K V V D I I Q G L D L L T A M 218
 721 GGTTCTGGTGAATCACATTTTCTTTAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATA 780
 219 V L V N H I F F K A K W E K P F H L E Y 238
 781 TACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT 840
 239 T R K N F P F L V G E Q V T V Q V P M M 258
 841 GCACCAGAAAGAGCAGTTCGCTTTTGGGGTGGATACAGAGCTGAACTGCTTTGTGCTGCA 900
 259 H Q K E Q F A F G V D T E L N C F V L Q 278

Figure 2

		1		50
AL132708_FL	(1)	MQQGRRRGTCCKDIFCSKMASYLYGV	FAVGLCAPIYCVSPANAPSAYPR	
AACT_HUMAN	(1)	-----	MERMLPLLALGLLAAGFCPAVLCHPNSPLD	
KAIN_HUMAN	(1)	-----	MHLIDYLLLLVGLLALSHGQLHVEHDGESC	
THBG_HUMAN	(1)	-----	MSPFLYLVLVLGLLHATIHCAPEGKVTACHS	
		51		100
AL132708_FL	(51)	PS-----	STKSTPASQVYSLNTDFAERLYRRLVLET	PSQNIFFSPVSV
AACT_HUMAN	(31)	EENLTQENQDRGTHVDLGLASANVDFA	SLYKQLVLKADKNVIFSPLSI	
KAIN_HUMAN	(33)	NSSHQQILETGEGSPSLKIAPANADFA	ERFYLIASETPGKNIFFSPLSI	
THBG_HUMAN	(33)	-----	SQPNATLYKMSSINADFAFNLYRRFTVET	PDKNIFFSPVSI
		101		150
AL132708_FL	(94)	STSLAMISLGAHSVTKQTLLQGLG	FNLTHTPESAIHQGFQHLVHSTIVPS	
AACT_HUMAN	(81)	STALAFISLGAHNTTLTETLKGLKFN	LTTETSEAEIHQSFOHLRTINQSS	
KAIN_HUMAN	(83)	SAAYAMISLGACSHSRQILEGLG	FNLTELSESDVHRGFQHLHTINLPG	
THBG_HUMAN	(74)	SAALVMSLFGACCSTQTEIVETL	GFNLTDTPMVEIQHGFQHLICSINFPK	
		151		200
AL132708_FL	(144)	KDITLKMGSALFVKKEQLQANFL	GNVKRLYEAEVSTDFSNPSIAQARI	
AACT_HUMAN	(131)	DELQLSMGNAMFVKEQSLLDRT	EDAKRLGSEAFATDFQDSAAAKKLI	
KAIN_HUMAN	(133)	HGLETRVGSALFLSHNLKFLAK	FLNDTMAVVEAKLEHINFYDTVGTIQL	
THBG_HUMAN	(124)	KELELQIGNALEFIGKHLKPLAK	FLNDVKTLYETEVSDFSNISAAKQET	
		201		250
AL132708_FL	(194)	NSHVKKKTQGVVDIIQGLDLLT	AMVLVNHITFFKAKWEKPEHLEYIRKNF	
AACT_HUMAN	(181)	NDYVKNGTGKITDLIKDLSQTM	VLVNYTFKAKWEMFDPQDTHQSR	
KAIN_HUMAN	(183)	NDHVKKETRGKIVDLVSEIKK	DVLMVLVNYTFKALWEKPEISSRTTPKD	
THBG_HUMAN	(174)	NSHVEMQTKGVVGLIQDKPNT	IMVLVNYTFKQAWANPEDPSKTEDSS	
		251		300
AL132708_FL	(244)	PFLVGEQVTVQVPMHMQEQFA	FGVIDEINCFVLQMDYKGDVAFFVLPS	
AACT_HUMAN	(231)	FYLSKKKWVMVPMSLHHLTIP	YFRDEELSCTVVELKYTGNASALFILPD	
KAIN_HUMAN	(233)	FYVDENTTVRVPMMLQDQEH	HWYLDHRYLPQSVLRMDYKGDATVFFILPN	
THBG_HUMAN	(224)	SFLIDKTTTVQVPMHMQEQY	HLVDMEINCFVLQMDYSKNALALFILPK	
		301		350
AL132708_FL	(294)	KGKMRQLEQALSARTLIKWSH	SFOKR---WIEVFIERFSISASYNDETI	
AACT_HUMAN	(281)	QDKMEEVEAMLLPETIKRWR	DSLEFR---EIGELYLPKFSISRDNLDNI	
KAIN_HUMAN	(283)	QGKMREIEVLTPEMLMRVNN	LKRNFYKKLEHLHPKFSISGSYVLDQI	
THBG_HUMAN	(274)	EGQMESVEAAMSSKTKKWN	RLQKG---WVDLFVPKEFSTSATYDLAGT	
		351		400
AL132708_FL	(340)	TPKMGIQNAFDKNADFSGL	IAKRDSIQVSKATHKAVLDVSEEGTEATAATT	
AACT_HUMAN	(328)	LLQLGIEEAFTSKADLSGIT	GARNIAVSQVVKAVLDVFEEGTEASAATA	
KAIN_HUMAN	(333)	LPRLGFTDLFSKWADLSGIT	KQKLEASKSFHKATLDVDEACTEAAAATT	
THBG_HUMAN	(320)	ILKMGIQHAYSENADFSGL	TEDNGLKLSNAAHKAVLHIGEKGTAAAVPE	
		401	↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓	446
AL132708_FL	(390)	TKFIVRSKDGPSYFTVSFNR	THLMMITNKATDGILFLGKVENPTKS	
AACT_HUMAN	(378)	VKITLLSALVETRTRIVRFN	PELMIIVPTDTQNIFFMSKVTNEKQA	
KAIN_HUMAN	(383)	FAIKFFSAQTN-RHILRFN	PELVVIFSTSTQSVLELGKVVDPETKP	
THBG_HUMAN	(370)	VELSDQPENTFLHPITQID	SEMLLILERSIRSIILGKVVNTEA	

Figure 3

LSI-01 pdb1qlp	MQGQRRRGT CKDIFCSKMA SYLYGVLFV GLCAPIYCVS PANAPSAYPR MDPQ GDAAQKTDTS
LSI-01 pdb1qlp	PSSTKSTPAS QVYSLNTDFA FRLYRRLVLE TPSQNIFFSP VSVSTSLAMD HHDQDHPTFN KITPNLAEFA FSLYRQLAHQ SNSTNIFFSP VSIATAFAMI
LSI-01 pdb1qlp	SLGAHSVTKT QILOGLGFNL THTPESAIHQ GFOHLVHSLT VPSKDLTKM SLGTKADTHD EILEGLNFNL TELPEAQIHE GFQELLRTLN QPDSQLQETT
LSI-01 pdb1qlp	GSALFVKKEI QLQANFLGNV KRLYEAEEVS TDFSNPSTIAQ ARINSHVKKK GNGLFLSEGL KLVDKELEDV KKLYHSEAF VNFQDTEEA KQINDYVEK
LSI-01 pdb1qlp	TQGVVDIIQ GLDLLTAMVL VNHIFFKAKW EKPFHLEYTR KNFPFLVGEQ TQGIYDLVK ELDRDTVFAL VNYIFFKQKW ERPFVKDT. EEEDFHVDQV
LSI-01 pdb1qlp	VTVQVEMMHQ KEQFAFGVDT ELNCFVLQMD YKGDVAFFV LPSKQKMRQ TTVKVEMMKR LGMFNIQHCK KLSWVLLMK YLGNATAIEF LPDEGKLQHL
LSI-01 pdb1qlp	EQALSARTLI KWSHSLQKRW IEVFIPRFST SASYNLETIL PKMGITQAFD ENELTHDIIT KFLNEDRRS ASLHLPLSLT TGTYDLKSVL GOLGITKVS
LSI-01 pdb1qlp	KNADFSGIK RDLSIQVSKAT HKAVLDVSEE GTEATAATT KFIVRSKDGP NGADLSGVTE EAPLKLSKAV HKAVLTIDEK GTEAAGAMFL EAIPMSI..P
LSI-01 pdb1qlp	S.YFTVSENR TELMMITNKA TDGILFLGKV ENPIKS PE...VKFNK PFVFLMIEQN TKSPLFMGRV VNPTQK

Figure 4.

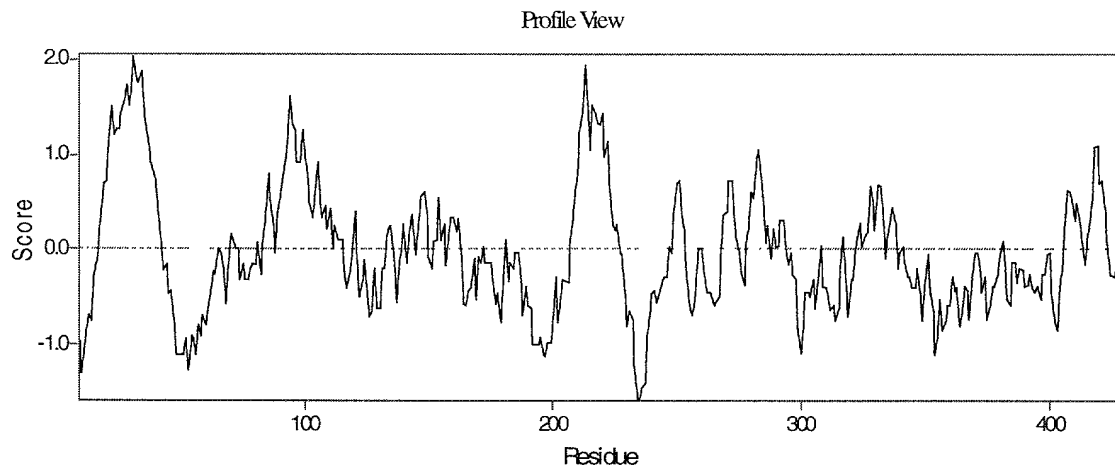


Figure 5.

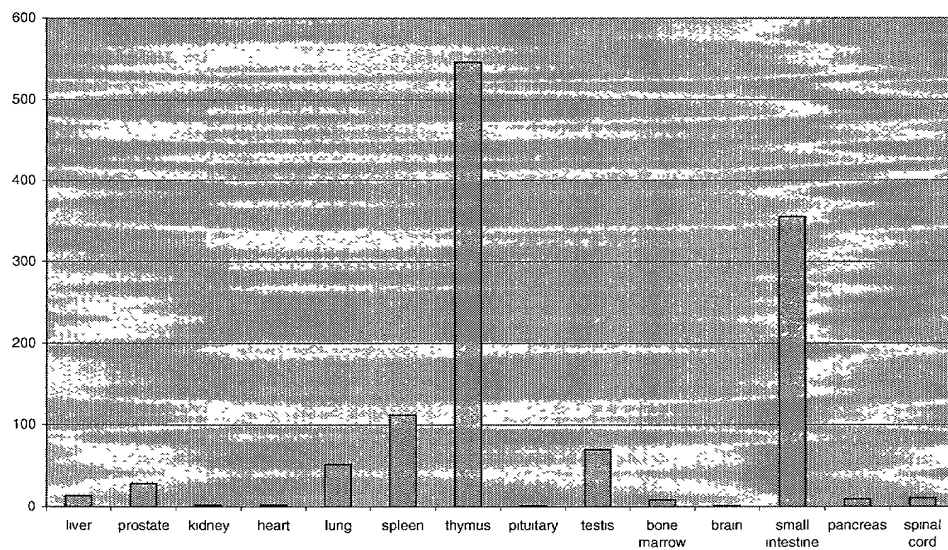
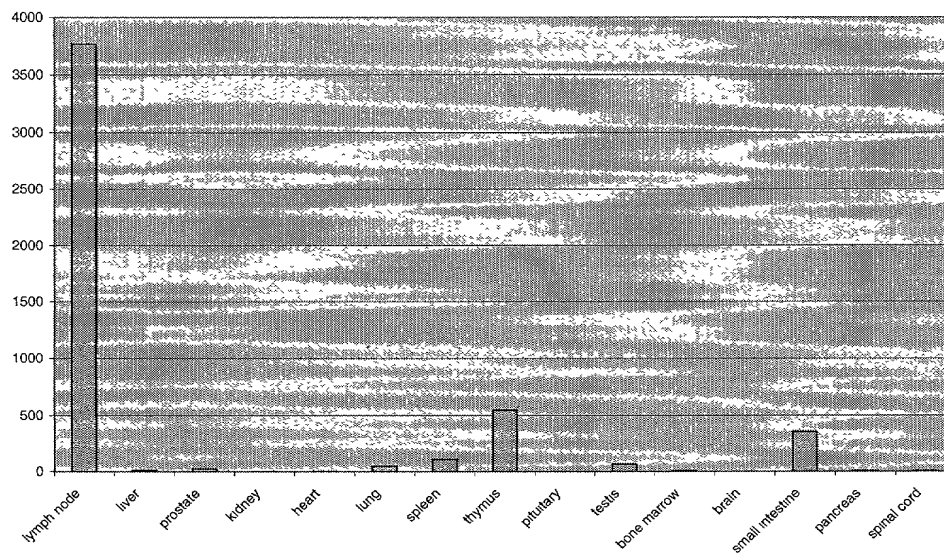


Figure 6.

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human α_1 -antichymotrypsin	gil112874	46%	52%
human Kallistatin	gil5453888	48%	56%
human thyroxin-binding globulin	gil37142	51%	57%
human α_1 -antithrypsin	gil6137432	43%	50%

Figure 7

